AMENDMENTS TO THE SPECIFICATION:

Please delete the paragraph bridging pages 15 and 16 of Applicants' specification, and substitute therefore the following new paragraph:

-- In order for the protein complex according to the present invention to have the F_0F_1-ATPase activity, each component protein of the protein complex has such identity to the corresponding amino acid sequences represented by each of SEQ ID NOS: 1 to 8, as at least 60%, preferably 80% or more, more preferably 95% or more. The identity of a nucleotide sequence or an amino acid sequence can be determined using the algorithm "BLAST" by Karlin and Altschl [Proc. Natl. Acad. Sci. USA, <u>90</u>, 5873-5877 (1993)]. The programs called "BLASTN" and "BLASTX" have been developed based on the above algorithm [J. Mol. Biol., <u>215</u>, 403-410 (1990)]. In the case of analyzing a nucleotide sequence based on BLAST, the parameter can be set to e.g. score=100, wordlength=12. In the case of analyzing an amino acid sequence based on BLASTX, the parameter can be set to e.g. score=50, wordlength=3. In the case of using BLAST or Gapped BLAST program, a default parameter of each program can be used. The specific analysis methods of using the above programs are known in the art ~~(http://www.ncbi.nlm.nih.gov.)~~(see www.ncbi.nlm.nih.gov). --